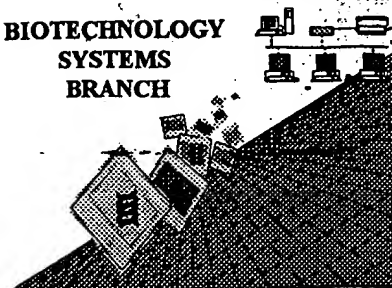


## **RAW SEQUENCE LISTING** **ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



0400  
#4

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/645,593

Source: OIPF

Date Processed by STIC: 9/7/2000

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER,  
703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER**  
**VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW:

RECEIVED  
SEP 20 2000  
OIPF/JCW

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**  
**<http://www.uspto.gov/web/offices/pac/checker>**

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/645,593

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2        Wrapped Aminos      The amino acid number/text at the end of each line "wrapped " down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3        Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4        Misaligned Amino Acid      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs  
Numbering      between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5        Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6        Variable Length      Sequence(s)        contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and  
indicate in the (ix) feature section that some may be missing.
- 7        PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
sequence(s)       . Normally, PatentIn would automatically generate this section from the  
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section  
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>  
sections for Artificial or Unknown sequences.
- 8        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence:  
(OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence.  
(NEW RULES)      <210> sequence id number  
                                 <400> sequence id number  
                                 000
- 10        Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11        Use of <213>Organism      Sequence(s)        are missing this mandatory field or its response.  
(NEW RULES)
- 12        Use of <220>Feature      Sequence(s)        are missing the <220>Feature and associated headings.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13        PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted  
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

P.7

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/645,593

DATE: 09/07/2000  
TIME: 14:27:09

Input Set : A:\Sequence  
Output Set: N:\CRF3\09072000\I645593.raw

Does Not Comply  
Corrected Diskette Needed

OK  
4 <110> APPLICANT: Chaudhary, Sarita  
5 van Rooijen, Gijs  
6 Moloney, Maurice  
7 Singh, Surinder  
9 <120> TITLE OF INVENTION: Flax Seed Specific Promoters  
11 <130> FILE REFERENCE: 9369-147  
13 <140> CURRENT APPLICATION NUMBER: US/09/645,593  
14 <141> CURRENT FILING DATE: 2000-08-25  
16 <150> PRIOR APPLICATION NUMBER: 60/151044  
17 <151> PRIOR FILING DATE: 1999-08-27  
19 <150> PRIOR APPLICATION NUMBER: 60/161,722  
20 <151> PRIOR FILING DATE: 1999-10-27  
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59 tcaaatgtgt attgtggact atgtgagcta atattgaacc tttatctctc ccaaccactc 1680

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/645,593

DATE: 09/07/2000  
TIME: 14:27:09

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62 aacatattct aagactacat gcatgcaaa tgcaaccctt gcatggaaag ctgctcaaca 1860
63 cgtggcatag actcccgcca cgtgtccatt ccacctcatt acctcaccct caccgttcac 1920
64 ctcttattat atcacaacaa tcaatcaatc ctactcctcc atactcgaac aaatccgacc 1980
65 aacttatacc aatattccca aacttgatta atttctcagc aatatggatc agacgcacca 2040
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67 gcagcagccg aggtcttacc aggcggtgaa ggcggccact gcagccaccg cgggtggatc 2160
68 cctcatcggt ctgtccggtc tcactcctac ggccaccgtc atttactca tcatagccac 2220
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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/645,593

DATE: 09/07/2000  
 TIME: 14:27:09

Input Set : A:\Sequence  
 Output Set: N:\CRF3\09072000\I645593.raw

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112 1 5 10 15
114 Tyr Gly Gly Gly Gly Thr Met Tyr Gln Gln Gln Pro Arg Ser Tyr
115 20 25 30
117 Gln Ala Val Lys Ala Ala Thr Ala Ala Thr Ala Gly Gly Ser Leu Ile
118 35 40 45
120 Val Leu Ser Gly Leu Ile Leu Thr Ala Thr Val Ile Ser Leu Ile Ile
121 50 55 60
123 Ala Thr Pro Leu Leu Val Ile Phe Ser Pro Val Leu Val Pro Ala Leu
124 65 70 75 80
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163 ccatacacacc acatataaag caatagtgtt ggagcttttc atatttgaaa cgggcattga 540
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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/645,593  
 DATE: 09/07/2000  
 TIME: 14:27:09

Input Set : A:\Sequence  
 Output Set: N:\CRF3\09072000\I645593.raw

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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/645,593

DATE: 09/07/2000  
 TIME: 14:27:09

Input Set : A:\Sequence  
 Output Set: N:\CRF3\09072000\I645593.raw

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234      65      70      75      80
236 Ile Thr Thr Pro Ile Phe Val Ile Cys Ser Pro Val Leu Val Pro Ala
237      85      90      95
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240      100     105     110
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243      115     120     125
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254 Ala Ser Asp Lys
255      180
258 <210> SEQ ID NO: 6
259 <211> LENGTH: 1676
260 <212> TYPE: DNA
261 <213> ORGANISM: Linum usitatissimum
263 <400> SEQUENCE: 6
264 tccactatgt aggtcatatc catcatttta atttttgggc accattcaat tccatcttgc 60
265 ctttagggat gtgaatatga acggccaagg taagagaata aaaataatcc aaattaaagc 120
266 aagagaggcc aagtaagata atccaaatgt acacttgta tcgccgaaat tagtaaaata 180
267 cgcggcatat tgtattccca cactattatta aaataaccgta tatgtattgg ctgcatttgc 240
268 atgaataata ctacgtgtaa gcccaaaaga acccacgtgt agcccatgca aagttaacac 300
269 tcacgacccc attcctcagt ctccactata taaacccacc atccccaatc ttaccaaacc 360
270 caccacacga ctcaacaetc gactctcaca ccttaaagaa ccaatcacca ccaaaaaatg 420
271 gcaaagctga tgagcctagc agccgtagca acgcagttcc tcttctctgat cgtggtggac 480
272 gcattccgtcc gaaccacagt gattatcgac gaggagacca accaaggccg cgtgaggagg 540
273 aaggtggcag ggacagcagc agtctgcgag cagcagatcc agcagcgaga ctctctgagg 600
274 agctgccagc agttcatgtg ggagaaagtc cagaggggag gccacagcca ctattacaac 660
275 cagggcgtg gagggagcga acagagccag tacttcgaac agctgtttgt gacgacctta 720
276 agcaattgag caccgcggtg caccatgcca ggggacttga agcgtgccat cggccaaatg 780
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281 tgtgttttaa gttagtgtaa cagctgtaat aaagagagag agagagagag agagagagag 1080
282 agagagagag agagagagag agaggctgat gaaatgttat gtatgtttct tggtttttaa 1140
283 aataaatgaa agcacatgct cgtgtggttc tatcgaatta ttccggcggt cctgtgggaa 1200
284 aaagtccaga agggcgccgc cagctactac tacaaccaag gccgtggagg agggcaacag 1260
285 agccagcact tcgatagctg ctgcgatgat cttaagcaat tgaggagcga gtgcacatgc 1320
286 aggggactgg agcgtgcaat cggccagatg aggcaggaca tccagcagca gggacagcag 1380
287 caggaagttg agaggtggtc ccatcaatct aaacaagtcg ctaggagacct tccgggacag 1440

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<210> 8  
<211> 4999  
<212> DNA  
<213> Linum usitatissimum

*see next page*

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caaacaaagc agaagacagg taatctttca tacttatact gacaagtaat agtcttaccg 660  
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|            |            |            |             |             |             |      |
|------------|------------|------------|-------------|-------------|-------------|------|
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| catgagacta | attgagaaca | tggcgatcc  | ttctcgggca  | gacattttca  | ctccagaagc  | 3180 |
| cggccgcgtt | agatccctca | acagccacaa | cctcccgctc  | ctgcaatgga  | tccagcttag  | 3240 |
| cgccgagaga | ggcgttctct | acaatgtata | gatctcactc  | acgcaccaac  | tctaaattga  | 3300 |
| atccctaatt | atttaattca | ccgatatctg | accgaccggt  | ttgaattttg  | taggaagcga  | 3360 |
| tcaggctgcc | gcactggaac | atcaacgcac | acagcatagt  | gtacgcgatc  | agaggacaag  | 3420 |
| ccagagtcca | gatcgtgaac | gaggaaggga | attcgggtgtt | cgatggagtg  | ctgcaggaag  | 3480 |
| gacaggtggt | gacggtgccg | cagaacttcg | cggtggtaaa  | gagatcccag  | agcgagaggt  | 3540 |
| ttgagtgggt | ggcgttcaag | accaacgaca | acgcgatggt  | gaactcgcta  | gccgggagga  | 3600 |
| catcggcagt | aagggcgatc | cccgcggatg | tactggctaa  | cgcctggagg  | gtgtcgccgg  | 3660 |
| aggaggcgag | gagggtgaag | ttcaacaggc | aggagactca  | cttggctagc  | accaggggcc  | 3720 |
| agtccaggtc | gcccgggagg | ttgaatgtcg | tcaaggaggt  | gatcaacttg  | cttatgtaaa  | 3780 |
| atgtgacggt | gaaataataa | cggtaaaata | tatgtaataa  | taataataat  | aaagccacaa  | 3840 |
| agtgagaatg | aggggaaggg | gaaatgtgta | atgagccagt  | agccgggtgtt | gctaattttg  | 3900 |
| tatcgtattg | tcaataaatc | atgaattttg | tggtttttat  | gtgttttttt  | aaatcatgaa  | 3960 |
| ttttaaat   | tataaaataa | tctccaatcg | gaagaacaac  | attccatata  | catggatgtt  | 4020 |
| tctttaccca | aatctagt   | ttgagaggat | gaagcatcac  | cgaacagttc  | tgcaactata  | 4080 |
| cctcaaaagc | tttaaaatga | acaacaagga | acagagcaac  | gttccaaaga  | tcccaaacga  | 4140 |
| aacatattat | ctataactat | actatattat | taattactac  | tgcccggaat  | cacaatccct  | 4200 |
| gaatgattcc | tattaactac | aagccttggt | ggcggcgagg  | aagtgatcgg  | cgccggcgaga | 4260 |
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| ttggggngcc | nanaggnagc | cncangggna | nnngcncnc   | ttgtncangn  | cgctnaagtt  | 4980 |
| cnattgtana | tggncgttg  |            |             |             |             | 4999 |

→ see  
den 10  
on  
Error  
summary  
sheet

Please explain all n's in the sequence. The circled n's are a sample.

FSI

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/645,593

DATE: 09/07/2000  
TIME: 14:27:10

Input Set : A:\Sequence  
Output Set: N:\CRF3\09072000\I645593.raw

L:13 M:270 C: Current Application Number differs, Replaced Application Number  
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:412 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8  
L:412 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8  
L:412 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8  
L:412 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8  
L:412 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8  
L:413 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8  
L:413 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8  
L:413 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8  
L:413 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8  
M:340 Repeated in SeqNo=8  
L:414 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8  
L:414 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8  
L:414 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8  
L:414 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8  
L:415 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8  
L:415 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8  
L:415 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8  
L:415 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8  
L:416 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8  
L:416 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8  
L:416 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8  
L:416 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8  
L:417 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8  
L:417 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8  
L:417 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8  
L:417 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8  
L:418 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8  
L:418 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8  
L:418 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8  
L:418 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8  
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L:421 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8  
L:422 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8  
L:422 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8  
L:422 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8  
L:422 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/645,593

DATE: 09/07/2000

TIME: 14:27:10

Input Set : A:\Sequence

Output Set: N:\CRF3\09072000\I645593.raw

L:455 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:10  
L:455 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10  
L:455 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10  
L:455 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10  
L:455 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10